



IFWO

RAW SEQUENCE LISTING

DATE: 08/16/2004

PATENT APPLICATION: US/10/698,808

TIME: 16:03:58

Input Set : N:\Crf4\Refhold\10_folder\J698808.raw

Output Set: N:\CRF4\08162004\J698808.raw

1 <110> APPLICANT: Adeokun, Anthonia Monisola
 2 Ambrose, Helen
 3 Cresswell, Carl
 4 Dudley, Adam
 5 <120> TITLE OF INVENTION: Chemical Compounds
 6 <130> FILE REFERENCE: 06275-264002
 7 <140> CURRENT APPLICATION NUMBER: US/10/698,808
 8 <141> CURRENT FILING DATE: 2003-10-03
 9 <150> PRIOR APPLICATION NUMBER: US 09/925,731
 10 <151> PRIOR FILING DATE: 2001-08-10
 11 <150> PRIOR APPLICATION NUMBER: US 60/226,909
 12 <151> PRIOR FILING DATE: 2000-08-23
 13 <160> NUMBER OF SEQ ID NOS: 12
 14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2452
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (100)...(2172)
 23 <400> SEQUENCE: 1
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 25 caacaacaaa aacatttgta tgatatctat atttcaatc atg gac caa aat caa 114
 26 Met Asp Gln Asn Gln
 27 1 5
 28 cat ttg aat aaa aca gca gag gca caa cct tca gag aat aag aaa aca 162
 29 His Leu Asn Lys Thr Ala Glu Ala Gln Pro Ser Glu Asn Lys Lys Thr
 30 10 15 20
 31 aga tac tgc aat gga ttg aag atg ttc ttg gca gct ctg tca ctc agc 210
 32 Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala Ala Leu Ser Leu Ser
 33 25 30 35
 34 ttt att gct aag aca cta ggt gca att att atg aaa agt tcc atc att 258
 35 Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met Lys Ser Ser Ile Ile
 36 40 45 50
 37 cat ata gaa cgg aga ttt gag ata tcc tct tct ctt gtt ggt ttt att 306
 38 His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser Leu Val Gly Phe Ile
 39 55 60 65
 40 gac gga agc ttt gaa att gga aat ttg ctt gtg att gta ttt gtg agt 354
 41 Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val Ile Val Phe Val Ser
 42 70 75 80 85
 43 tac ttt gga tcc aaa cta cat aga cca aag tta att gga atc ggt tgt 402
 44 Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu Ile Gly Ile Gly Cys



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45				90				95				100					
46	ttc	att	atg	gga	att	gga	ggt	gtt	ttg	act	gct	ttg	cca	cat	ttc	ttc	450
47	Phe	Ile	Met	Gly	Ile	Gly	Gly	Val	Leu	Thr	Ala	Leu	Pro	His	Phe	Phe	
48				105				110				115					
49	atg	gga	tat	tac	agg	tat	tct	aaa	gaa	act	aat	atc	aat	tca	tca	gaa	498
50	Met	Gly	Tyr	Tyr	Arg	Tyr	Ser	Lys	Glu	Thr	Asn	Ile	Asn	Ser	Ser	Glu	
51				120				125				130					
52	aat	tca	aca	tcg	acc	tta	tcc	act	tgt	tta	att	aat	caa	att	tta	tca	546
53	Asn	Ser	Thr	Ser	Thr	Leu	Ser	Thr	Cys	Leu	Ile	Asn	Gln	Ile	Leu	Ser	
54				135				140				145					
55	ctc	aat	aga	gca	tca	cct	gag	ata	gtg	gga	aaa	ggt	tgt	tta	aag	gaa	594
56	Leu	Asn	Arg	Ala	Ser	Pro	Glu	Ile	Val	Gly	Lys	Gly	Cys	Leu	Lys	Glu	
57				150				155				160				165	
58	tct	ggg	tca	tac	atg	tgg	ata	tat	gtg	ttc	atg	ggt	aat	atg	ctt	cgt	642
59	Ser	Gly	Ser	Tyr	Met	Trp	Ile	Tyr	Val	Phe	Met	Gly	Asn	Met	Leu	Arg	
60				170				175				180					
61	gga	ata	ggg	gag	act	ccc	ata	gta	cca	ctg	ggg	ctt	tct	tac	att	gat	690
62	Gly	Ile	Gly	Glu	Thr	Pro	Ile	Val	Pro	Leu	Gly	Leu	Ser	Tyr	Ile	Asp	
63				185				190				195					
64	gat	ttc	gct	aaa	gaa	gga	cat	tct	tct	ttg	tat	tta	ggt	ata	ttg	aat	738
65	Asp	Phe	Ala	Lys	Glu	Gly	His	Ser	Ser	Leu	Tyr	Leu	Gly	Ile	Leu	Asn	
66				200				205				210					
67	gca	ata	gca	atg	att	ggt	cca	atc	att	ggc	ttt	acc	ctg	gga	tct	ctg	786
68	Ala	Ile	Ala	Met	Ile	Gly	Pro	Ile	Ile	Gly	Phe	Thr	Leu	Gly	Ser	Leu	
69				215				220				225					
70	ttt	tct	aaa	atg	tac	gtg	gat	att	gga	tat	gta	gat	cta	agc	act	atc	834
71	Phe	Ser	Lys	Met	Tyr	Val	Asp	Ile	Gly	Tyr	Val	Asp	Leu	Ser	Thr	Ile	
72				230				235				240				245	
73	agg	ata	act	cct	act	gat	tct	cga	tgg	gtt	gga	gct	tgg	tgg	ctt	aat	882
74	Arg	Ile	Thr	Pro	Thr	Asp	Ser	Arg	Trp	Val	Gly	Ala	Trp	Trp	Leu	Asn	
75				250				255				260					
76	ttc	ctt	gtg	tct	gga	cta	ttc	tcc	att	tct	tcc	ata	cca	ttc	ttt		930
77	Phe	Leu	Val	Ser	Gly	Leu	Phe	Ser	Ile	Ser	Ser	Ile	Pro	Phe	Phe		
78				265				270				275					
79	ttc	ttg	ccc	caa	act	cca	aat	aaa	cca	caa	aaa	gaa	aga	aaa	gct	tca	978
80	Phe	Leu	Pro	Gln	Thr	Pro	Asn	Lys	Pro	Gln	Lys	Glu	Arg	Lys	Ala	Ser	
81				280				285				290					
82	ctg	tct	ttg	cat	gtg	ctg	gaa	aca	aat	gat	gaa	aag	gat	caa	aca	gct	1026
83	Leu	Ser	Leu	His	Val	Leu	Glu	Thr	Asn	Asp	Glu	Lys	Asp	Gln	Thr	Ala	
84				295				300				305					
85	aat	ttg	acc	aat	caa	gga	aaa	aat	att	acc	aaa	aat	gtg	act	ggt	ttt	1074
86	Asn	Leu	Thr	Asn	Gln	Gly	Lys	Asn	Ile	Thr	Lys	Asn	Val	Thr	Gly	Phe	
87				310				315				320				325	
88	ttc	cag	tct	ttt	aaa	agc	atc	ctt	act	aat	ccc	ctg	tat	gtt	atg	ttt	1122
89	Phe	Gln	Ser	Phe	Lys	Ser	Ile	Leu	Thr	Asn	Pro	Leu	Tyr	Val	Met	Phe	
90				330				335				340					
91	gtg	ctt	ttg	acg	ttg	tta	caa	gta	agc	agc	tat	att	ggt	gct	ttt	act	1170
92	Val	Leu	Leu	Thr	Leu	Leu	Gln	Val	Ser	Ser	Tyr	Ile	Gly	Ala	Phe	Thr	
93				345				350				355					

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94	tat gtc ttc aaa tac gta gag caa cag tat ggt cag cct tca tct aag	1218
95	Tyr Val Phe Lys Tyr Val Glu Gln Tyr Gly Gln Pro Ser Ser Lys	
96	360 365 370	
97	gct aac atc tta ttg gga gtc ata acc ata cct att ttt gca agt gga	1266
98	Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro Ile Phe Ala Ser Gly	
99	375 380 385	
100	atg ttt tta gga gga tat atc att aaa aaa ttc aaa ctg aac acc gtt	1314
101	Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe Lys Leu Asn Thr Val	
102	390 395 400 405	
103	gga att gcc aaa ttc tca tgt ttt act gct gtg atg tca ttg tcc ttt	1362
104	Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val Met Ser Leu Ser Phe	
105	410 415 420	
106	tac cta tta tat ttt ttc ata ctc tgt gaa aac aaa tca gtt gcc gga	1410
107	Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn Lys Ser Val Ala Gly	
108	425 430 435	
109	cta acc atg acc tat gat gga aat aat cca gtg aca tct cat aga gat	1458
110	Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val Thr Ser His Arg Asp	
111	440 445 450	
112	gta cca ctt tct tat tgc aac tca gac tgc aat tgt gat gaa agt caa	1506
113	Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn Cys Asp Glu Ser Gln	
114	455 460 465	
115	tgg gaa cca gtc tgt gga aac aat gga ata act tac atc tca ccc tgt	1554
116	Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr Tyr Ile Ser Pro Cys	
117	470 475 480 485	
118	cta gca ggt tgc aaa tct tca agt ggc aat aaa aag cct ata gtg ttt	1602
119	Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys Lys Pro Ile Val Phe	
120	490 495 500	
121	tac aac tgc agt tgt ttg gaa gta act ggt ctc cag aac aga aat tac	1650
122	Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu Gln Asn Arg Asn Tyr	
123	505 510 515	
124	tca gcc cat ttg ggt gaa tgc cca aga gat gat gct tgt aca agg aaa	1698
125	Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp Ala Cys Thr Arg Lys	
126	520 525 530	
127	ttt tac ttt ttt gtt gca ata caa gtc ttg aat tta ttt ttc tct gca	1746
128	Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn Leu Phe Phe Ser Ala	
129	535 540 545	
130	ctt gga ggc acc tca cat gtc atg ctg att gtt aaa att gtt caa cct	1794
131	Leu Gly Gly Thr Ser His Val Met Leu Ile Val Lys Ile Val Gln Pro	
132	550 555 560 565	
133	gaa ttg aaa tca ctt gca ctg ggt ttc cac tca atg gtt ata cga gca	1842
134	Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser Met Val Ile Arg Ala	
135	570 575 580	
136	cta gga gga att cta gct cca ata tat ttt ggg gct ctg att gat aca	1890
137	Leu Gly Gly Ile Leu Ala Pro Ile Tyr Phe Gly Ala Leu Ile Asp Thr	
138	585 590 595	
139	acg tgt ata aag tgg tcc acc aac aac tgt ggc aca cgt ggg tca tgt	1938
140	Thr Cys Ile Lys Trp Ser Thr Asn Asn Cys Gly Thr Arg Gly Ser Cys	
141	600 605 610	
142	agg aca tat aat tcc aca tca ttt tca agg gtc tac ttg ggc ttg tct	1986

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143 Arg Thr Tyr Asn Ser Thr Ser Phe Ser Arg Val Tyr Leu Gly Leu Ser
144      615                      620                      625
145 tca atg tta aga gtc tca tca ctt gtt tta tat att ata tta att tat      2034
146 Ser Met Leu Arg Val Ser Ser Leu Val Leu Tyr Ile Ile Leu Ile Tyr
147      630                      635                      640                      645
148 gcc atg aag aaa aaa tat caa gag aaa gat atc aat gca tca gaa aat      2082
149 Ala Met Lys Lys Lys Tyr Gln Glu Lys Asp Ile Asn Ala Ser Glu Asn
150      650                      655                      660
151 gga agt gtc atg gat gaa gca aac tta gaa tcc tta aat aaa aat aaa      2130
152 Gly Ser Val Met Asp Glu Ala Asn Leu Glu Ser Leu Asn Lys Asn Lys
153      665                      670                      675
154 cat ttt gtc cct tct gct ggg gca gat agt gaa aca cat tgt      2172
155 His Phe Val Pro Ser Ala Gly Ala Asp Ser Glu Thr His Cys
156      680                      685                      690
157 taaggggaga aaaaaagcca cttctgcttc tgtgtttcca aacagcattg cattgattca      2232
158 gtaagatggt atttttgagg agttcctggt cctttcacta agaatttcca catcttttat      2292
159 ggtggaagta taaataagcc tatgaactta taataaaaca aactgtaggt agaaaaaatg      2352
160 agagtactca ttgtacatta tagctacata tttgtgggta aggttagact atatgatcca      2412
161 taaaattaa agtgagagac atggttactg tgtaataaaa      2452
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164 <211> LENGTH: 691
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 2
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169      1      5      10      15
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171      20      25      30
172 Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
173      35      40      45
174 Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
175      50      55      60
176 Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
177      65      70      75      80
178 Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
179      85      90      95
180 Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
181      100      105      110
182 Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
183      115      120      125
184 Ile Asn Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
185      130      135      140
186 Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
187      145      150      155      160
188 Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
189      165      170      175
190 Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
191      180      185      190
192 Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr

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197		225				230					235					240
198	Asp	Leu	Ser	Thr	Ile	Arg	Ile	Thr	Pro	Thr	Asp	Ser	Arg	Trp	Val	Gly
199					245					250					255	
200	Ala	Trp	Trp	Leu	Asn	Phe	Leu	Val	Ser	Gly	Leu	Phe	Ser	Ile	Ile	Ser
201				260					265					270		
202	Ser	Ile	Pro	Phe	Phe	Phe	Leu	Pro	Gln	Thr	Pro	Asn	Lys	Pro	Gln	Lys
203			275					280					285			
204	Glu	Arg	Lys	Ala	Ser	Leu	Ser	Leu	His	Val	Leu	Glu	Thr	Asn	Asp	Glu
205		290					295					300				
206	Lys	Asp	Gln	Thr	Ala	Asn	Leu	Thr	Asn	Gln	Gly	Lys	Asn	Ile	Thr	Lys
207		305				310					315					320
208	Asn	Val	Thr	Gly	Phe	Phe	Gln	Ser	Phe	Lys	Ser	Ile	Leu	Thr	Asn	Pro
209					325					330					335	
210	Leu	Tyr	Val	Met	Phe	Val	Leu	Leu	Thr	Leu	Leu	Gln	Val	Ser	Ser	Tyr
211				340					345					350		
212	Ile	Gly	Ala	Phe	Thr	Tyr	Val	Phe	Lys	Tyr	Val	Glu	Gln	Gln	Tyr	Gly
213			355					360					365			
214	Gln	Pro	Ser	Ser	Lys	Ala	Asn	Ile	Leu	Leu	Gly	Val	Ile	Thr	Ile	Pro
215		370					375					380				
216	Ile	Phe	Ala	Ser	Gly	Met	Phe	Leu	Gly	Gly	Tyr	Ile	Ile	Lys	Lys	Phe
217		385				390					395					400
218	Lys	Leu	Asn	Thr	Val	Gly	Ile	Ala	Lys	Phe	Ser	Cys	Phe	Thr	Ala	Val
219					405					410					415	
220	Met	Ser	Leu	Ser	Phe	Tyr	Leu	Leu	Tyr	Phe	Phe	Ile	Leu	Cys	Glu	Asn
221				420					425					430		
222	Lys	Ser	Val	Ala	Gly	Leu	Thr	Met	Thr	Tyr	Asp	Gly	Asn	Asn	Pro	Val
223			435					440					445			
224	Thr	Ser	His	Arg	Asp	Val	Pro	Leu	Ser	Tyr	Cys	Asn	Ser	Asp	Cys	Asn
225		450					455					460				
226	Cys	Asp	Glu	Ser	Gln	Trp	Glu	Pro	Val	Cys	Gly	Asn	Asn	Gly	Ile	Thr
227		465				470					475					480
228	Tyr	Ile	Ser	Pro	Cys	Leu	Ala	Gly	Cys	Lys	Ser	Ser	Ser	Gly	Asn	Lys
229					485					490					495	
230	Lys	Pro	Ile	Val	Phe	Tyr	Asn	Cys	Ser	Cys	Leu	Glu	Val	Thr	Gly	Leu
231				500					505					510		
232	Gln	Asn	Arg	Asn	Tyr	Ser	Ala	His	Leu	Gly	Glu	Cys	Pro	Arg	Asp	Asp
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VERIFICATION SUMMARY

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